

10347-WO-ST25
SEQUENCE LISTING

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<170> PatentIn version 3.2

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 Asp Thr Leu Tyr Asp Ala Val Asp Asn Gly Ala Lys Gly Ile Val Val
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 Arg Ser Val Ser Ser Gly Tyr Tyr Asp Ala Ile
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 Asp Asp Ile Ala Ser Thr His Ser Leu Pro Val Val Leu Ser Thr Arg
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 Thr Gly Asn Gly Glu Val Ala Ile Thr Asp Ser Glu Thr Thr Ile Glu
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35 40 45

Asn Thr Thr Leu Pro Asn Val Thr Ile Leu Ala Thr Gly Gly Thr Ile
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Ala Gly Ser Ser Asn Asp Asn Thr Ala Thr Thr Gly Tyr Thr Ala Gly
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Page 10

370

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Thr		Thr		Gly		Tyr		Gln		Ala		Gly		Ala		Leu		Gly		Ile		Gln		Ala		Leu		Ile		Asp		
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His Ala Asn Ala Val Gln Thr Phe Ile Ala Glu Asp Gln Gly Tyr Leu	
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ggt gcc ttt gaa aac att cag ccc gtc ttc tgg tac cct gct agt cga	836
Gly Ala Phe Glu Asn Ile Gln Pro Val Phe Trp Tyr Pro Ala Ser Arg	
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Pro Leu Gly His His Tyr Phe Asn Ile Ser Ala Ser Ser Pro Lys Lys	
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Asn Ile Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Gly
 50 55 60

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 Gly Val Gln Ile Ala Asn Val Asp Ser Gly Asp Val Asn Ser Thr Ile
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 Ile Gln Gly Val Val Val Thr His Gly Thr Asp Thr Leu Glu Glu Ser
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 Asn Leu Leu Ser Ala Val Arg Leu Ala Gly Ser Lys Ser Ala Lys Gly
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 Gln Gly Tyr Leu Gly Ala Phe Glu Asn Ile Gln Pro Val Phe Trp Tyr
 225 230 235 240
 Pro Ala Ser Arg Pro Leu Gly His His Tyr Phe Asn Ile Ser Ala Ser
 245 250 255
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 260 265 270
 Glu Ala Asp Pro Glu Leu Phe Gln Ala Ala Val Asp Ser Gly Ala Gln
 275 280 285
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 95 100 105
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Val Ser Val Trp Gly Ser Pro Val Leu Asp Leu His Val Gln Pro His
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Val Thr Ile Tyr Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Ser Ser
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Arg Thr Leu Ala Lys Gln Ile Gln Asn Asp Leu Asp Ser Pro Phe Thr
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Gln Gly Ala Val Val Thr His Gly Thr Asp Thr Leu Asp Glu Ser Ala
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 Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Met Asn
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 245 250 255
 Gly Val Met Ile Ala Met Asn Asp Arg Ile Gly Ser Ala Arg Phe Thr
 260 265 270
 Thr Lys Val Asn Ala Asn His Leu Asp Ala Phe Gln Ala Pro Asp Ser
 275 280 285
 Gly Met Leu Gly Thr Phe Val Asn Val Gln Pro Val Phe Phe Tyr Pro
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 Pro Ser Arg Pro Leu Gly His Arg His Phe Asp Leu Arg Pro Ile Thr
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 Asn Asn Gly Arg Arg Phe Gly Arg Ser Thr Ala Pro Gly Ala Gly Ser
 325 330 335
 Ser Ala Leu Pro Gln Val Asp Val Leu Tyr Ala Tyr Gln Glu Leu Ser
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 Val Gly Met Phe Gln Ala Ala Ile Asp Leu Gly Ala Gln Gly Ile Val
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 Leu Ala Gly Met Gly Ala Gly Phe Trp Thr Ser Lys Gly Thr Glu Glu
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 385 390 395 400
 Arg Pro Glu Gly Gly Phe Val Gly Pro Cys Glu Ala Gly Ile Gly Ala
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Ala Ser Leu Pro Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala		
	45 50 55 60	
ggt aca agc gat gac aag act gct acg gca gga tat gaa tcc ggg gct	243	
Gly Thr Ser Asp Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala		
	65 70 75	
tta ggg ata aat aag att ctt tcc ggc atc cca gaa gtt tat gac att	291	
Leu Gly Ile Asn Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile		
	80 85 90	
gcc aac gtc aat gcg gta cag ttt gac aat gtc aac agc ggc gat gtc	339	
Ala Asn Val Asn Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val		
	95 100 105	
tct yca tct ctc tta ctg aac atg aca cat acc ctt caa aag acc gtt	387	
Ser Xaa Ser Leu Leu Leu Asn Met Thr His Thr Leu Gln Lys Thr Val		
	110 115 120	
tgt gat gac cct acg ata tct ggc gcc gtc atc acc cat ggc acc gat	435	
Cys Asp Asp Pro Thr Ile Ser Gly Ala Val Ile Thr His Gly Thr Asp		
	125 130 135 140	
acc ctg gaa gaa tct gcc ttc ttc atc gat gca aca gtc aac tgc ggc	483	
Thr Leu Glu Glu Ser Ala Phe Phe Ile Asp Ala Thr Val Asn Cys Gly		
	145 150 155	
aag ccg att gtg ttc gtt ggc tca atg cga cct tcc acc gca atc tct	531	
Lys Pro Ile Val Phe Val Gly Ser Met Arg Pro Ser Thr Ala Ile Ser		
	160 165 170	
gcc gat ggc cct atg aat ttg ctc cag gga gtg act gtg gcc gct gac	579	
Ala Asp Gly Pro Met Asn Leu Leu Gln Gly Val Thr Val Ala Ala Asp		
	175 180 185	
aaa cag gct aag aac cgc gga gca cta gtc gtg ctg aat gac cgc att	627	
Lys Gln Ala Lys Asn Arg Gly Ala Leu Val Val Leu Asn Asp Arg Ile		
	190 195 200	
gtc tct gct ttc ttc gct aca aag aca aat gcg aat aca atg gac act	675	
Val Ser Ala Phe Phe Ala Thr Lys Thr Asn Ala Asn Thr Met Asp Thr		
	205 210 215 220	
ttc aag gct tat gaa caa ggc agt ctt ggc atg att gtt tca aac aag	723	
Phe Lys Ala Tyr Glu Gln Gly Ser Leu Gly Met Ile Val Ser Asn Lys		
	225 230 235	

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ccc tac ttc tat tat ccg gca gtc gag cca aac gcg aag cac gtt gtt	771
Pro Tyr Phe Tyr Tyr Pro Ala Val Glu Pro Asn Ala Lys His Val Val	
240 245 250	
cat ctt gac gac gtg gat gcg atc ccc cgt gtg gat att ctc tac gct	819
His Leu Asp Asp Val Asp Ala Ile Pro Arg Val Asp Ile Leu Tyr Ala	
255 260 265	
tac gag gac atg cat agc gac tcc ctt cac agt gct atc aaa aat gga	867
Tyr Glu Asp Met His Ser Asp Ser Leu His Ser Ala Ile Lys Asn Gly	
270 275 280	
gcc aag ggc atc gtg gtc gcc ggc gag ggc gca ggt ggt atc tcc acg	915
Ala Lys Gly Ile Val Val Ala Gly Glu Gly Ala Gly Gly Ile Ser Thr	
285 290 295	
gac ttt agt gat acc atc gat gag att gca tcg aag cat cag att ccc	963
Asp Phe Ser Asp Thr Ile Asp Glu Ile Ala Ser Lys His Gln Ile Pro	
305 310 315	
att atc ctg agc cac aga acc gtg aac gga gaa gtt cct act gct gat	1011
Ile Ile Leu Ser His Arg Thr Val Asn Gly Glu Val Pro Thr Ala Asp	
320 325 330	
att acg ggt gat agc gcg aag act cgc att gca agt ggc atg tat aac	1059
Ile Thr Gly Asp Ser Ala Lys Thr Arg Ile Ala Ser Gly Met Tyr Asn	
335 340 345	
ccc cag cag gcg cgc gtc ttg ctt gga cta ttg ctc gca gaa ggc aag	1107
Pro Gln Gln Ala Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys	
350 355 360	
aag ttt gag gat att cga act atc ttc gga aaa gct act gtt gcc	1152
Lys Phe Glu Asp Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala	
365 370 375	
tagaccacg tcatatatta tgccatact tgggaaact tgaaactgat agactaaatt	1212
aattatattg tcgtttgttg ccgg	1236

<210> 12
 <211> 379
 <212> PRT
 <213> Penicillium citrinum

<220>
 <221> misc_feature
 <222> (110)..(110)
 <223> The 'xaa' at location 110 stands for Pro, or Ser.

<400> 12

Met Arg Leu Leu Phe Asn Thr Leu Ala Val Ser Ala Leu Ala Ala Thr
 1 5 10 15

Ser Tyr Ala Ser Pro Ile Ile His Ser Arg Ala Ser Asn Thr Ser Tyr
 20 25 30

Thr Asn Ser Asn Gly Leu Lys Phe Asn His Phe Asp Ala Ser Leu Pro
 35 40 45

Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala Gly Thr Ser Asp
 50 55 60

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Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala Leu Gly Ile Asn
 65 70 75 80
 Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile Ala Asn Val Asn
 85 90 95
 Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val Ser Xaa Ser Leu
 100 105 110
 Leu Leu Asn Met Thr His Thr Leu Gln Lys Thr Val Cys Asp Asp Pro
 115 120 125
 Thr Ile Ser Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
 130 135 140
 Ser Ala Phe Phe Ile Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
 145 150 155 160
 Phe Val Gly Ser Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
 165 170 175
 Met Asn Leu Leu Gln Gly Val Thr Val Ala Ala Asp Lys Gln Ala Lys
 180 185 190
 Asn Arg Gly Ala Leu Val Val Leu Asn Asp Arg Ile Val Ser Ala Phe
 195 200 205
 Phe Ala Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Tyr
 210 215 220
 Glu Gln Gly Ser Leu Gly Met Ile Val Ser Asn Lys Pro Tyr Phe Tyr
 225 230 235 240
 Tyr Pro Ala Val Glu Pro Asn Ala Lys His Val Val His Leu Asp Asp
 245 250 255
 Val Asp Ala Ile Pro Arg Val Asp Ile Leu Tyr Ala Tyr Glu Asp Met
 260 265 270
 His Ser Asp Ser Leu His Ser Ala Ile Lys Asn Gly Ala Lys Gly Ile
 275 280 285
 Val Val Ala Gly Glu Gly Ala Gly Gly Ile Ser Thr Asp Phe Ser Asp
 290 295 300
 Thr Ile Asp Glu Ile Ala Ser Lys His Gln Ile Pro Ile Ile Leu Ser
 305 310 315 320
 His Arg Thr Val Asn Gly Glu Val Pro Thr Ala Asp Ile Thr Gly Asp
 325 330 335

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Ser Ala Lys Thr Arg Ile Ala Ser Gly Met Tyr Asn Pro Gln Gln Ala
 340 345 350

Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys Lys Phe Glu Asp
 355 360 365

Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala
 370 375

<210> 13

<211> 362

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 13

Met Arg Ser Leu Asn Thr Leu Leu Leu Ser Leu Phe Val Ala Met Ser
 1 5 10 15

Ser Gly Ala Pro Leu Leu Lys Ile Arg Glu Glu Lys Asn Ser Ser Leu
 20 25 30

Pro Ser Ile Lys Ile Phe Gly Thr Gly Gly Thr Ile Ala Ser Lys Gly
 35 40 45

Ser Thr Ser Ala Thr Thr Ala Gly Tyr Ser Val Gly Leu Thr Val Asn
 50 55 60

Asp Leu Ile Glu Ala Val Pro Ser Leu Ala Glu Lys Ala Asn Leu Asp
 65 70 75 80

Tyr Leu Gln Val Ser Asn Val Gly Ser Asn Ser Leu Asn Tyr Thr His
 85 90 95

Leu Ile Pro Leu Tyr His Gly Ile Ser Glu Ala Leu Ala Ser Asp Asp
 100 105 110

Tyr Ala Gly Ala Val Val Thr His Gly Thr Asp Thr Met Glu Glu Thr
 115 120 125

Ala Phe Phe Leu Asp Leu Thr Ile Asn Ser Glu Lys Pro Val Cys Ile
 130 135 140

Ala Gly Ala Met Arg Pro Ala Thr Ala Thr Ser Ala Asp Gly Pro Met
 145 150 155 160

Asn Leu Tyr Gln Ala Val Ser Ile Ala Ala Ser Glu Lys Ser Leu Gly
 165 170 175

Arg Gly Thr Met Ile Thr Leu Asn Asp Arg Ile Ala Ser Gly Phe Trp
 180 185 190

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Thr Thr Lys Met Asn Ala Asn Ser Leu Asp Thr Phe Arg Ala Asp Glu
 195 200 205

Gln Gly Tyr Leu Gly Tyr Phe Ser Asn Asp Asp Val Glu Phe Tyr Tyr
 210 215 220

Pro Pro Val Lys Pro Asn Gly Trp Gln Phe Phe Asp Ile Ser Asn Leu
 225 230 235 240

Thr Asp Pro Ser Glu Ile Pro Glu Val Ile Ile Leu Tyr Ser Tyr Gln
 245 250 255

Gly Leu Asn Pro Glu Leu Ile Val Lys Ala Val Lys Asp Leu Gly Ala
 260 265 270

Lys Gly Ile Val Leu Ala Gly Ser Gly Ala Gly Ser Trp Thr Ala Thr
 275 280 285

Gly Ser Ile Val Asn Glu Gln Leu Tyr Glu Glu Tyr Gly Ile Pro Ile
 290 295 300

Val His Ser Arg Arg Thr Ala Asp Gly Thr Val Pro Pro Asp Asp Ala
 305 310 315 320

Pro Glu Tyr Ala Ile Gly Ser Gly Tyr Leu Asn Pro Gln Lys Ser Arg
 325 330 335

Ile Leu Leu Gln Leu Cys Leu Tyr Ser Gly Tyr Gly Met Asp Gln Ile
 340 345 350

Arg Ser Val Phe Ser Gly Val Tyr Gly Gly
 355 360

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Primer AoASP7

<400> 14
 caaggatcca gcagtatggg tgtcaatttc

30

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> Primer AoASP8

<400> 15
 atcaagcttc tattatccat cccatcca

28